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=> s 11q13/ti and pygm/ti
L1 5 11Q13/TI AND PYGM/TI

=> d 1-5 ti

L1 ANSWER 1 OF 5 MEDLINE
TI The germinal center kinase gene and a novel CDC25-like gene are located in the vicinity of the **PYGM** gene on **11q13**.

L1 ANSWER 2 OF 5 MEDLINE
TI Localization of the photoreceptor gene ROM1 to human chromosome 11 and mouse chromosome 19: sublocalization to human **11q13** between PGA and **PYGM**.

L1 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI The germinal center kinase gene and a novel CDC25-like gene are located in the vicinity of the **PYGM** gene on **11q13**.

L1 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Localization of the photoreceptor gene ROM1 to human chromosome 11 and mouse chromosome 19: Sublocalization to human **11q13** between PGA and **PYGM**.

L1 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2003 ACS
TI The germinal center kinase gene and a novel CDC25-like gene are located in the vicinity of the **PYGM** gene on **11q13**

=> d bib ab

L1 ANSWER 1 OF 5 MEDLINE
AN 1998001089 MEDLINE
DN 98001089 PubMed ID: 9341881
TI The germinal center kinase gene and a novel CDC25-like gene are located in the vicinity of the **PYGM** gene on **11q13**.
AU Kedra D; Seroussi E; Fransson I; Trifunovic J; Clark M; Lagercrantz J; Blennow E; Mehlin H; Dumanski J
CS Department of Molecular Medicine, Karolinska Hospital, Stockholm, Sweden.
SO HUMAN GENETICS, (1997 Oct) 100 (5-6) 611-9.
Journal code: 7613873. ISSN: 0340-6717.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
OS GENBANK-Y12334; GENBANK-Y12335; GENBANK-Y12336; GENBANK-Y12337; GENBANK-Y12338; GENBANK-Y12339
EM 199711
ED Entered STN: 19971224
Last Updated on STN: 20020420
Entered Medline: 19971119
AB Multiple endocrine neoplasia type 1 (MEN1) is tightly linked to the muscle-type glycogen phosphorylase (PYGM) gene in 11q13. This region of the human genome contains additional disease-related loci implicated in the development of insulin-dependent diabetes mellitus, familial paraganglioma type 2, spinocerebellar ataxia type 5, Bardet-Biedl syndrome and translocation t(11;17) described in B-cell non-Hodgkin's lymphoma. We approached cloning of candidate disease genes from 11q13 by large-scale genomic sequencing. We obtained > 106 kb of sequence around the PYGM gene and established a transcriptional map that includes: (i) two genes previously localized to 11q13, PYGM and a zinc-finger protein (ZFM1) gene; (ii) the germinal center kinase (GCK, human B-lymphocyte serine/threonine protein kinase) gene; (iii) a novel human CDC25-like (HCDC25L) gene; (iv) a dystrophia myotonica protein kinase-like (DMPKL) gene; and (v) a novel ubiquitously expressed gene of unknown function (germinal center kinase-neighboring gene, GCKNG).

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 08:49:30 ON 12 FEB 2003
L1 5 S 11Q13/TI AND PYGM/TI

=> s 11q13 and bac
L2 42 11Q13 AND BAC

=> s l2 and ac000134
L3 0 L2 AND AC000134

=> s ac000134
L4 3 AC000134

=> d 1-3 ti

L4 ANSWER 1 OF 3 MEDLINE
TI Analysis of the human neurexin genes: alternative splicing and the generation of protein diversity.

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS
TI Eighteen new polymorphic markers in the multiple endocrine neoplasia type 1 (MEN1) region

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS
TI A transcript map for the 2.8-Mb region containing the multiple endocrine neoplasia type 1 locus

=> d 1-3 bib ab

L4 ANSWER 1 OF 3 MEDLINE
AN 2002211495 MEDLINE
DN 21945268 PubMed ID: 11944992
TI Analysis of the human neurexin genes: alternative splicing and the generation of protein diversity.

AU Rowen Lee; Young Janet; Birditt Brian; Kaur Amardeep; Madan Anup; Philipps Dana L; Qin Shizhen; Minx Patrick; Wilson Richard K; Hood Leroy; Graveley Brenton R

CS Institute for Systems Biology, 1441 North 34th Street, Seattle, Washington 98103, USA.

SO GENOMICS, (2002 Apr) 79 (4) 587-97.
Journal code: 8800135. ISSN: 0888-7543.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-**AC000134**

EM 200208

ED Entered STN: 20020412
Last Updated on STN: 20020817
Entered Medline: 20020816

AB The neurexins are neuronal proteins that function as cell adhesion molecules during synaptogenesis and in intercellular signaling. Although mammalian genomes contain only three neurexin genes, thousands of neurexin isoforms may be expressed through the use of two alternative promoters and alternative splicing at up to five different positions in the pre-mRNA. To begin understanding how the expression of the neurexin genes is regulated, we have determined the complete nucleotide sequence of all three human neurexin genes: NRXN1, NRXN2, and NRXN3. Unexpectedly, two of these, NRXN1 (approximately 1.1 Mb) and NRXN3 (approximately 1.7 Mb), are among the largest known human genes. In addition, we have identified several conserved intronic sequence elements that may participate in the regulation of alternative splicing. The sequences of these genes provide insight into the mechanisms used to generate the diversity of neurexin protein isoforms and raise several interesting questions regarding the expression mechanism of large genes.

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS

AN 1997:638125 CAPLUS

DN 128:44394

TI Eighteen new polymorphic markers in the multiple endocrine neoplasia type 1 (MEN1) region

AU Manickam, Pachiappan; Guru, Siradanahalli C.; Debelenko, Larisa V.; Agarwal, Sunita K.; Olufemi, Shodimu-Emmanuel; Weisemann, Jane M.; Boguski, Mark S.; Crabtree, Judy S.; Wang, Yingping; Roe, Bruce A.; Lubensky, Irina A.; Zhuang, Zhengping; Kester, Mary Beth; Burns, A. Lee; Spiegel, Allen M.; Marx, Stephen J.; Liotta, Lance A.; Emmert-Buck, Michael R.; Collins, Francis S.; Chandrasekharappa, S. C.

CS NIH, Laboratory of Pathology, National Cancer Institute, Bethesda, 20 892, MD, USA

SO Human Genetics (1997), 101(1), 102-108
CODEN: HUGEDQ; ISSN: 0340-6717

PB Springer

DT Journal

LA English

AB Multiple endocrine neoplasia type 1 (MEN1) is an autosomal dominant disorder in which affected individuals develop tumors primarily in the parathyroids, anterior pituitary, endocrine pancreas, and duodenum. The locus for MEN1 is tightly linked to the marker PYGM on chromosome 11q13, and linkage anal. has previously placed the MEN1 gene within a 2-Mb interval flanked by markers D11S1883 and D11S449. Loss of heterozygosity (LOH) studies in MEN1 and sporadic tumors have helped narrow the location of the gene to a 600-kb interval between PYGM and D11S449. Eighteen new polymerase chain reaction (PCR)-based polymorphic markers were generated for the MEN1 region, with ten mapping to the PYGM-D11S449 interval. These new markers, along with 14 previously known polymorphic markers, were precisely mapped on a 2.8-Mb (D11S480-D11S913) high-d. clone contig-based,

phys. map generated for the MEN1 region.

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS
AN 1997:523238 CAPLUS
DN 127:230150
TI A transcript map for the 2.8-Mb region containing the multiple endocrine neoplasia type 1 locus
AU Guru, Siradanahalli C.; Agarwal, Sunita K.; Manickam, Pachiappan; Olufemi, Shodimu-Emmanuel; Crabtree, Judy S.; Weisemann, Jane M.; Kester, Mary Beth; Kim, Young S.; Wang, Yingping; Emmert-Buck, Michael R.; Liotta, Lance A.; Spiegel, Allen M.; Boguski, Mark S.; Roe, Bruce A.; Collins, Francis S.; Marx, Stephen J.; Burns, Lee; Chandrasekharappa, Settara C.
CS Lab. Gene Transfer, Metabolic Dis. Branch, Natl. Library Med., Lab. Pathology, Natl. Human Genome Res. Inst., Natl. Inst. Diabetes and Digestive and Kidney Diseases, Natl. Cancer Inst., Natl. Inst. Health, Bethesda, MD, 20892, USA
SO Genome Research (1997), 7(7), 725-735
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Multiple endocrine neoplasia type 1 (MEN 1) is an inherited cancer syndrome in which affected individuals develop multiple parathyroid, enteropancreatic, and pituitary tumors. The locus for MEN1 is tightly linked to the marker PYGM on chromosome 11q13, and linkage anal. places the MEN1 gene within a 2-Mb interval flanked by the markers D11S1883 and D11S449. Loss of heterozygosity studies in MEN 1 and sporadic tumors suggest that the MEN1 gene encodes a tumor suppressor and have helped to narrow the location of the gene to a 600-kb interval between PYGM and D11S449. Focusing on this smaller MEN1 interval, the authors have identified and mapped 12 transcripts to this 600-kb region. A precise ordered map of 33 transcripts, including 12 genes known to map to this region, was generated for the 2.8-Mb D11S480-D11S913 interval. Fifteen candidate genes (of which 10 were examd. exhaustively) were evaluated by Southern blot and/or dideoxy fingerprinting anal. to identify the gene harboring disease-causing mutations.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	18.13	18.34

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LAST RELOADED: Feb 7, 2003 (20030207/UP).

=> file medline

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.08	19.42

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION

CA SUBSCRIBER PRICE 0.00 -1.30

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FILE LAST UPDATED: 11 FEB 2003 (20030211/UP). FILE COVERS 1958 TO DATE.

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MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/summ2003.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s pan?/au and ptcf/ti
56146 PAN?/AU
1 PTCF/TI
L5 1 PAN?/AU AND PTCF/TI

=> d bib

L5 ANSWER 1 OF 1 MEDLINE
AN 95226129 MEDLINE
DN 95226129 PubMed ID: 7710784
TI The complete nucleotide sequences of the SacBII Kan domain of the P1 pAD10-SacBII cloning vector and three cosmid cloning vectors: **pTCF**, svPHEP, and LAWRIST16.
AU **Pan H Q**; Wang Y P; Chissoe S L; Bodenteich A; Wang Z; Iyer K; Clifton S W; Crabtree J S; Roe B A
CS Department of Chemistry and Biochemistry, University of Oklahoma, Norman 73019.
SO GENETIC ANALYSIS, TECHNIQUES AND APPLICATIONS, (1994) 11 (5-6) 181-6. Journal code: 9004550. ISSN: 1050-3862.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L19898; GENBANK-L19899; GENBANK-L19900
EM 199505
ED Entered STN: 19950524
Last Updated on STN: 19980206
Entered Medline: 19950512

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.54	19.96

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-1.30

FILE 'STNGUIDE' ENTERED AT 09:02:13 ON 12 FEB 2003

FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Feb 7, 2003 (20030207/UP).

=> d 1 bib ab
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L5 ANSWER 1 OF 1 MEDLINE
AN 95226129 MEDLINE
DN 95226129 PubMed ID: 7710784
TI The complete nucleotide sequences of the SacBII Kan domain of the P1 pAD10-SacBII cloning vector and three cosmid cloning vectors: **pTCF**, svPHEP, and LAWRIST16.
AU **Pan H Q**; Wang Y P; Chissoe S L; Bodenteich A; Wang Z; Iyer K; Clifton S W; Crabtree J S; Roe B A
CS Department of Chemistry and Biochemistry, University of Oklahoma, Norman 73019.
SO GENETIC ANALYSIS, TECHNIQUES AND APPLICATIONS, (1994) 11 (5-6) 181-6. Journal code: 9004550. ISSN: 1050-3862.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L19898; GENBANK-L19899; GENBANK-L19900
EM 199505
ED Entered STN: 19950524
Last Updated on STN: 19980206
Entered Medline: 19950512
AB The complete nucleotide sequence of the 16,009-bp SacBII Kan domain of the P1 pAD10-SacBII cloning vector and the sequences of three cosmid cloning vectors, pTCF (7941 bp), svPHEP (9201 bp), and LAWRIST16 (5194 bp) have been determined. A modified diatomaceous earth (Prep-A-Gene)-based procedure, which rapidly yields highly supercoiled double-stranded DNA from recombinant P1 and cosmid clones suitable for generating shotgun libraries, also has been developed. The isolated recombinant DNAs were physically sheared to generate 1- to 2-kb fragments that then were blunt-ended and subcloned into double-stranded pUC-based sequencing vectors. The double-stranded sequencing templates were isolated by an alkaline lysis method and subjected to Taq polymerase catalyzed fluorescent end-labeled primer cycle sequencing. After shotgun sequence assembly, contig gaps were closed and ambiguities were resolved via Sequenase catalyzed fluorescent dye-terminator sequencing.